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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/839,073

DATE: 03/21/2003

TIME: 13:05:05

Input Set : A:\13492.seq.txt

Output Set: N:\CRF4\03212003\I839073.raw

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3 <110> APPLICANT: Sacktor, Todd C.
5 <120> TITLE OF INVENTION: A MEMORY ENHANCING PROTEIN
7 <130> FILE REFERENCE: The Research Foundation Albany
9 <140> CURRENT APPLICATION NUMBER: 09/839,073
C--> 10 <141> CURRENT FILING DATE: 2003-03-17
12 <160> NUMBER OF SEQ ID NOS: 4
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2058
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (444)..(1670)
25 <220> FEATURE:
26 <221> NAME/KEY: unsure
27 <222> LOCATION: (522)
28 <223> OTHER INFORMATION: r at position 522 is g or a
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33 ttccgttaaa tatctgctcc tcgcgctcga gcctccctgc ctattgtcgg ggccggagcg 120
35 aagccgacgc agcatcagct cgtcaacggg aaggaagatg cctccctgca cgcccggcg 180
37 gcacagagca taaagaatct gcgctgagga ggcaggagaa gaaagccgaa tctatctacc 240
39 gccggggagc cagaagatgg aggaagctgt accgtgccaa cggccacctc ttccaagcca 300
41 agcgttttaa caggagagcg tactgcggtc agtgcagcga gaggatatgg ggctcgcga 360
43 ggcaaggcta caggatgcac aactgcaaac tgctggtcca taagcgtcgc cacggcctcg 420
45 tcccgtgac ctgcaggaag cat atg gat tct gtc atg cct tcc caa gag cct 473
46 Met Asp Ser Val Met Pro Ser Gln Glu Pro
47 1 5 10
49 cca gta gac gac aag aac gag gac gcc gac ctt cct tcc gag gag aca 521
50 Pro Val Asp Asp Lys Asn Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr
51 15 20 25
53 rat gga att gct tac att tcc tca tcc cgg aag cat gac agc att aaa 569
W--> 54 Xaa Gly Ile Ala Tyr Ile Ser Ser Ser Arg Lys His Asp Ser Ile Lys
55 30 35 40
57 gac gac tcg gag gac ctt aag cca gtt atc gat ggg atg gat gga atc 617
58 Asp Asp Ser Glu Asp Leu Lys Pro Val Ile Asp Gly Met Asp Gly Ile
59 45 50 55
61 aaa atc tct cag ggg ctt ggg ctg cag gac ttt gac cta atc aga gtc 665
62 Lys Ile Ser Gln Gly Leu Gly Leu Gln Asp Phe Asp Leu Ile Arg Val
63 60 65 70
66 atc ggg cgc ggg agc tac gcc aag gtt ctc ctg gtg cgg ttg aag aag 713
67 Ile Gly Arg Gly Ser Tyr Ala Lys Val Leu Leu Val Arg Leu Lys Lys

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68	75	80	85	90	
70	aat gac caa att tac gcc atg aaa gtg gtg aag aaa gag ctg gtg cat	761			
71	Asn Asp Gln Ile Tyr Ala Met Lys Val Val Lys Lys Glu Leu Val His				
72		95	100	105	
74	gat gac gag gat att gac tgg gta cag aca gag aag cac gtg ttt gag	809			
75	Asp Asp Glu Asp Ile Asp Trp Val Gln Thr Glu Lys His Val Phe Glu				
76		110	115	120	
78	cag gca tcc agc aac ccc ttc ctg gtc gga tta cac tcc tgc ttc cag	857			
79	Gln Ala Ser Ser Asn Pro Phe Leu Val Gly Leu His Ser Cys Phe Gln				
80		125	130	135	
82	acg aca agt cgg ttg ttc ctg gtc att gag tac gtc aac ggc ggg gac	905			
83	Thr Thr Ser Arg Leu Phe Leu Val Ile Glu Tyr Val Asn Gly Gly Asp				
84		140	145	150	
86	ctg atg ttc cac atg cag agg cag agg aag ctc cct gag gag cac gcc	953			
87	Leu Met Phe His Met Gln Arg Gln Arg Lys Leu Pro Glu Glu His Ala				
88	155	160	165	170	
90	agg ttc tac gcg gcc gag atc tgc atc gcc ctc aac ttc ctg cac gag	1001			
91	Arg Phe Tyr Ala Ala Glu Ile Cys Ile Ala Leu Asn Phe Leu His Glu				
92		175	180	185	
94	agg ggg atc atc tac agg gac ctg aag ctg gac aac gtc ctc ctg gat	1049			
95	Arg Gly Ile Ile Tyr Arg Asp Leu Lys Leu Asp Asn Val Leu Leu Asp				
96		190	195	200	
98	gcg gac ggg cac atc aag ctc aca gac tac ggc atg tgc aag gaa ggc	1097			
99	Ala Asp Gly His Ile Lys Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly				
100		205	210	215	
102	ctg ggc cct ggt gac aca acg agc act ttc tgc gga acc ccg aat tac	1145			
103	Leu Gly Pro Gly Asp Thr Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr				
104		220	225	230	
106	atc gcc ccc gaa atc ctg cgg gga gag gag tac ggg ttc agc gtg gac	1193			
107	Ile Ala Pro Glu Ile Leu Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp				
108	235	240	245	250	
110	tgg tgg gcg ctg gga gtc ctc atg ttt gag atg atg gcc ggg cgc tcc	1241			
111	Trp Trp Ala Leu Gly Val Leu Met Phe Glu Met Met Ala Gly Arg Ser				
112		255	260	265	
114	ccg ttc gac atc atc acc gac aac ccg gac atg aac aca gag gac tac	1289			
115	Pro Phe Asp Ile Ile Thr Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr				
116		270	275	280	
118	ctt ttc caa gtg atc ctg gag aag ccc atc cgg atc ccc cgg ttc ctg	1337			
119	Leu Phe Gln Val Ile Leu Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu				
120		285	290	295	
122	tcc gtc aaa gcc tcc cat gtt tta aaa gga ttt tta aat aag gac ccc	1385			
123	Ser Val Lys Ala Ser His Val Leu Lys Gly Phe Leu Asn Lys Asp Pro				
124		300	305	310	
126	aaa gag agg ctc ggc tgc cgg cca cag act gga ttt tct gac atc aag	1433			
127	Lys Glu Arg Leu Gly Cys Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys				
128	315	320	325	330	
131	tcc cac gcg ttc ttc cgc agc ata gac tgg gac ttg ctg gag aag aag	1481			
132	Ser His Ala Phe Phe Arg Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys				
133		335	340	345	

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135 cag gcg ctc cct cca ttc cag cca cag atc aca gac gac tac ggt ctg 1529
136 Gln Ala Leu Pro Pro Phe Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu
137          350          355          360
139 gac aac ttt gac aca cag ttc acc agc gag ccc gtg cag ctg acc cca 1577
140 Asp Asn Phe Asp Thr Gln Phe Thr Ser Glu Pro Val Gln Leu Thr Pro
141          365          370          375
143 gac gat gag gat gcc ata aag agg atc gac cag tca gag ttc gaa ggc 1625
144 Asp Asp Glu Asp Ala Ile Lys Arg Ile Asp Gln Ser Glu Phe Glu Gly
145          380          385          390
147 ttt gag tat atc aac cca tta ttg ctg tcc acc gag gag tcg gtg 1670
148 Phe Glu Tyr Ile Asn Pro Leu Leu Leu Ser Thr Glu Glu Ser Val
149 395          400          405
151 tgaggccgcg tgcgtctctg tcgtggacac gcgtgattga ccctttaact gtatccttaa 1730
153 ccaccgcata tgcattgccag gctgggcacg gctccgaggg cgccagggga cagacgcttg 1790
155 cgccgagacc gcagagggaa gcgtcagcgg gcgtgctggg gagcagaaca gtccttcaca 1850
157 cctggcccg gaggcagctt cgtgctggag gaacttgcctg ctgtgcctgc gtcgcggcgg 1910
159 atccgcgggg accctgccga gggggctgtc atgcggtttc caaggtgcac attttccacg 1970
161 gaaacagaac tcgatgcact gacctgctcc gccaggaaaag tgagcgtgta gcgtcctgag 2030
163 gaataaaatg ttccgatgaa aaaaaaaaaa 2058
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 409
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <220> FEATURE:
172 <221> NAME/KEY: unsure
173 <222> LOCATION: (27)
174 <223> OTHER INFORMATION: Xaa at position 27 is Asp or Asn
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179 1 5 10 15
W--> 181 Glu Asp Ala Asp Leu Pro Ser Glu Glu Thr Xaa Gly Ile Ala Tyr Ile
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184 Ser Ser Ser Arg Lys His Asp Ser Ile Lys Asp Asp Ser Glu Asp Leu
185          35          40          45
187 Lys Pro Val Ile Asp Gly Met Asp Gly Ile Lys Ile Ser Gln Gly Leu
188          50          55          60
190 Gly Leu Gln Asp Phe Asp Leu Ile Arg Val Ile Gly Arg Gly Ser Tyr
191 65          70          75          80
193 Ala Lys Val Leu Leu Val Arg Leu Lys Lys Asn Asp Gln Ile Tyr Ala
194          85          90          95
196 Met Lys Val Val Lys Lys Glu Leu Val His Asp Asp Glu Asp Ile Asp
197          100          105          110
199 Trp Val Gln Thr Glu Lys His Val Phe Glu Gln Ala Ser Ser Asn Pro
200          115          120          125
202 Phe Leu Val Gly Leu His Ser Cys Phe Gln Thr Thr Ser Arg Leu Phe
203          130          135          140
205 Leu Val Ile Glu Tyr Val Asn Gly Gly Asp Leu Met Phe His Met Gln
206 145          150          155          160
208 Arg Gln Arg Lys Leu Pro Glu Glu His Ala Arg Phe Tyr Ala Ala Glu

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209          165          170          175
211 Ile Cys Ile Ala Leu Asn Phe Leu His Glu Arg Gly Ile Ile Tyr Arg
212          180          185          190
214 Asp Leu Lys Leu Asp Asn Val Leu Leu Asp Ala Asp Gly His Ile Lys
215          195          200          205
217 Leu Thr Asp Tyr Gly Met Cys Lys Glu Gly Leu Gly Pro Gly Asp Thr
218          210          215          220
220 Thr Ser Thr Phe Cys Gly Thr Pro Asn Tyr Ile Ala Pro Glu Ile Leu
221 225          230          235          240
223 Arg Gly Glu Glu Tyr Gly Phe Ser Val Asp Trp Trp Ala Leu Gly Val
224          245          250          255
226 Leu Met Phe Glu Met Met Ala Gly Arg Ser Pro Phe Asp Ile Ile Thr
227          260          265          270
229 Asp Asn Pro Asp Met Asn Thr Glu Asp Tyr Leu Phe Gln Val Ile Leu
230          275          280          285
232 Glu Lys Pro Ile Arg Ile Pro Arg Phe Leu Ser Val Lys Ala Ser His
233          290          295          300
235 Val Leu Lys Gly Phe Leu Asn Lys Asp Pro Lys Glu Arg Leu Gly Cys
236 305          310          315          320
238 Arg Pro Gln Thr Gly Phe Ser Asp Ile Lys Ser His Ala Phe Phe Arg
239          325          330          335
241 Ser Ile Asp Trp Asp Leu Leu Glu Lys Lys Gln Ala Leu Pro Pro Phe
242          340          345          350
244 Gln Pro Gln Ile Thr Asp Asp Tyr Gly Leu Asp Asn Phe Asp Thr Gln
245          355          360          365
247 Phe Thr Ser Glu Pro Val Gln Leu Thr Pro Asp Asp Glu Asp Ala Ile
248          370          375          380
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258 <210> SEQ ID NO: 3
259 <211> LENGTH: 2058
261 <212> TYPE: DNA
262 <213> ORGANISM: Homo sapiens
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267 ttcggctgcg tcgtagtcga gcagttgccc ttctttctac ggagggacgt gcgggcggcg 180
268 cgtgtctcgt atttcttaga cgcgactcct ccgtcctctt ctttcggctt agatagatgg 240
269 cggcccctcg gtctttctacc tccttcgaca tggcacgggt gccgggtggag aagggttcgg 300
270 tcgcgaaaatt gtcctctcgc atgacgccag tcacgtcgtc ctcctatacc ccggagcgct 360
271 ccgttccgat gtccacgtag ttgacgtttg acgaccagggt attcgcgacg gtgccggagc 420
272 agggcgactg gacgtccttc gtatacctaa gacagtacgg aagggttctc ggaggtcatc 480
273 tgctgttctt gctcctgcgg ctggaaggaa ggctcctctg tctaccttaa cgaatgtaaa 540
274 gagtagggc cttcgtactg tcgtaatttc tgctgagcct cctggaattc ggtcaatagc 600
275 taccctacct accttagttt tagagagtcc ccgaaccoga cgtcctgaaa ctggattagt 660
276 ctcahtagcc cgcgccctcg atgcggttcc aagaggacca cgccaacttc ttcttactgg 720
277 tttaaatgcg gtactttcac cacttctttc tcgaccacgt actactgctc ctataactga 780

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Input Set : A:\13492.seq.txt

Output Set: N:\CRF4\03212003\I839073.raw

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280 ccctggacta caaggtgtac gtctccgtct ccttcgaggg actcctcgtg cggccaaga 960
281 tgcgccggct ctagacgtag cgggagttga aggacgtgct ctccccctag tagatgtccc 1020
282 tggacttcga cctgttgca gaggacctac gcctgccgt gtagtccgag tgtctgatgc 1080
283 cgtacacgtt ccttcggac cgggaccac tgtgttgctc gtgaaagacg ccttggggct 1140
284 taatgtagcg ggggttttag gacgccctc tcctcatgcc caagtcgcac ctgaccaccc 1200
285 gcgaccctca ggagtacaaa ctctactacc ggcccgcgag gggcaagctg tagtagtggc 1260
286 tggtgggcct gtacttgtgt ctctgatgg aaaaggttca ctaggacctc ttcgggtagg 1320
287 cctagggggc caaggacagg cagtttcgga ggtacaaaa ttttcctaaa aatttattcc 1380
288 tggggtttct ctccgagccg acggccggtg tctgacctaa aagactgtag ttcagggtgc 1440
289 gcaagaaggc gtcgtatctg accctgaacg acctcttctt cgtccgcgag ggaggttaag 1500
290 tcggtgtcta gtgtctgctg atgccagacc tgttgaaact gtgtgtcaag tggtcgctcg 1560
291 ggcacgtcga ctgggggtctg ctactcctac ggtatttctc ctactgtggtc agtctcaagc 1620
292 ttccgaaaact catatagttg ggtaataacg acagggtggc cctcagccac actccggcgc 1680
293 acgcagagac agcacctgtg cgcactaact gggaaattga cataggaatt ggtggcgtat 1740
294 acgtacggtc cgaccctgtc cgaggctccc gccggtccct gtctgcgaac gcggctctgg 1800
296 cgtctccctt cgcagtcgcc cgcgacgacc ctctcttctt caggaggtgt ggaccgggcc 1860
297 gtccgtcgaa gcacgacctc cttgaacgac gacacggacg cagcgcgcgc taggcgcccc 1920
298 tgggacggct ccccgacag tacgccaaag gttccacgtg taaaagggtg ctttgtcttg 1980
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300 aaggctactt tttttttt 2058
303 <210> SEQ ID NO: 4
304 <211> LENGTH: 13
305 <212> TYPE: PRT
306 <213> ORGANISM: Unknown Organism
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Unknown Organism: mzip peptide
311 <400> SEQUENCE: 4
312 Ser Ile Tyr Arg Arg Gly Ala Arg Arg Trp Arg Lys Leu
313 1 5 10

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 03/21/2003

PATENT APPLICATION: US/09/839,073

TIME: 13:05:06

Input Set : A:\13492.seq.txt

Output Set: N:\CRF4\03212003\I839073.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 27

Seq#:2; Xaa Pos. 27

VERIFICATION SUMMARY

DATE: 03/21/2003

PATENT APPLICATION: **US/09/839,073**

TIME: 13:05:06

Input Set : **A:\13492.seq.txt**Output Set: **N:\CRF4\03212003\I839073.raw**

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:54 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:569

L:181 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:16